

MOR0277.ST25.txt  
SEQUENCE LISTING

<110> Nicolaides, Nicholas C.  
Grasso, Luigi  
Sass, Philip M. M.

<120> METHOD FOR GENERATING GENETICALLY ALTERED ANTIGENS

<130> MOR-0277

<150> US 09/712,691  
<151> 2000-11-14

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<170> PatentIn version 3.2

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<212> PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 5

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 35 40 45

Ala Gly Ala Thr Thr Ile Asp Leu Arg Leu Lys Asp Tyr Gly Val Asp  
 50 55 60

Leu Ile Glu Val Ser Asp Asn Gly Cys Gly Val Glu Glu Glu Asn Phe  
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Glu Gly Leu Ala Leu Lys His His Thr Ser Lys Ile Gln Glu Phe Ala  
 85 90 95

Asp Leu Thr Gln Val Glu Thr Phe Gly Phe Arg Gly Glu Ala Leu Ser  
 100 105 110

Ser Leu Cys Ala Leu Ser Asp Val Thr Ile Ser Thr Cys His Gly Ser  
 115 120 125

Ala Ser Val Gly Thr Arg Leu Val Phe Asp His Asn Gly Lys Ile Thr  
 130 135 140

Gln Lys Thr Pro Tyr Pro Arg Pro Lys Gly Thr Thr Val Ser Val Gln  
 145 150 155 160

His Leu Phe Tyr Thr Leu Pro Val Arg Tyr Lys Glu Phe Gln Arg Asn  
 165 170 175

Ile Lys Lys Glu Tyr Ser Lys Met Val Gln Val Leu Gln Ala Tyr Cys  
 180 185 190

Ile Ile Ser Ala Gly Val Arg Val Ser Cys Thr Asn Gln Leu Gly Gln  
 195 200 205

Gly Lys Arg His Ala Val Val Cys Thr Ser Gly Thr Ser Gly Met Lys  
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Glu Asn Ile Gly Ser Val Phe Gly Gln Lys Gln Leu Gln Ser Leu Ile  
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Pro Phe Val Gln Leu Pro Pro Ser Asp Ala Val Cys Glu Glu Tyr Gly  
 245 250 255

Leu Ser Thr Ser Gly Arg His Lys Thr Phe Ser Thr Phe Arg Ala Ser  
 260 265 270

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 Leu Ser Met Arg Phe Tyr His Met Tyr Asn Arg His Gln Tyr Pro Phe  
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 Thr Pro Asp Lys Arg Gln Ile Leu Leu Gln Glu Glu Lys Leu Leu Leu  
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Pro Gly Thr Gly Gln Ser Leu Lys Pro Glu Asp His Gly Tyr Gln Cys  
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Lys Ala Leu Pro Leu Ala Arg Leu Ser Pro Thr Asn Ala Lys Arg Phe  
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Lys Thr Glu Glu Arg Pro Ser Asn Val Asn Ile Ser Gln Arg Leu Pro  
 580 585 590

Gly Pro Gln Ser Thr Ser Ala Ala Glu Val Asp Val Ala Ile Lys Met  
 595 600 605

Asn Lys Arg Ile Val Leu Leu Glu Phe Ser Leu Ser Ser Leu Ala Lys  
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Arg Met Lys Gln Leu Gln His Leu Lys Ala Gln Asn Lys His Glu Leu  
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Ser Tyr Arg Lys Phe Arg Ala Lys Ile Cys Pro Gly Glu Asn Gln Ala  
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Met Glu Ile Leu Gly Gln Phe Asn Leu Gly Phe Ile Val Thr Lys Leu  
 675 680 685

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Thr Ser Lys Asn Trp Thr Phe Gly Pro Gln Asp Ile Asp Glu Leu Ile  
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Arg Gln Met Phe Ala Ser Arg Ala Cys Arg Lys Ser Val Met Ile Gly  
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Thr Ala Leu Asn Ala Ser Glu Met Lys Lys Leu Ile Thr His Met Gly  
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 35 40 45

Ala Gly Ala Thr Asn Ile Asp Leu Lys Leu Lys Asp Tyr Gly Val Asp  
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Leu Ile Glu Val Ser Asp Asn Gly Cys Gly Val Glu Glu Glu Asn Phe  
 65 70 75 80  
 Glu Gly Leu Thr Leu Lys His His Thr Ser Lys Ile Gln Glu Phe Ala  
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 Asp Leu Thr Gln Val Glu Thr Phe Gly Phe Arg Gly Glu Ala Leu Ser  
 100 105 110  
 Ser Leu Cys Ala Leu Ser Asp Val Thr Ile Ser Thr Cys His Ala Ser  
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 Ala Lys Val Gly Thr Arg Leu Met Phe Asp His Asn Gly Lys Ile Ile  
 130 135 140  
 Gln Lys Thr Pro Tyr Pro Arg Pro Arg Gly Thr Thr Val Ser Val Gln  
 145 150 155 160  
 Gln Leu Phe Ser Thr Leu Pro Val Arg His Lys Glu Phe Gln Arg Asn  
 165 170 175  
 Ile Lys Lys Glu Tyr Ala Lys Met Val Gln Val Leu His Ala Tyr Cys  
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 Ile Ile Ser Ala Gly Ile Arg Val Ser Cys Thr Asn Gln Leu Gly Gln  
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 Gly Lys Arg Gln Pro Val Val Cys Thr Gly Gly Ser Pro Ser Ile Lys  
 210 215 220  
 Glu Asn Ile Gly Ser Val Phe Gly Gln Lys Gln Leu Gln Ser Leu Ile  
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 Pro Phe Val Gln Leu Pro Pro Ser Asp Ser Val Cys Glu Glu Tyr Gly  
 245 250 255  
 Leu Ser Cys Ser Asp Ala Leu His Asn Leu Phe Tyr Ile Ser Gly Phe  
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 Ile Ser Gln Cys Thr His Gly Val Gly Arg Ser Ser Thr Asp Arg Gln  
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 Phe Phe Phe Ile Asn Arg Arg Pro Cys Asp Pro Ala Lys Val Cys Arg  
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 Val Val Leu Asn Ile Ser Val Asp Ser Glu Cys Val Asp Ile Asn Val  
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Ala Val Leu Lys Thr Ser Leu Ile Gly Met Phe Asp Ser Asp Val Asn  
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Lys Leu Asn Val Ser Gln Gln Pro Leu Leu Asp Val Glu Gly Asn Leu  
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Ile Lys Met His Ala Ala Asp Leu Glu Lys Pro Met Val Glu Lys Gln  
 385 390 395 400

Asp Gln Ser Pro Ser Leu Arg Thr Gly Glu Glu Lys Lys Asp Val Ser  
 405 410 415

Ile Ser Arg Leu Arg Glu Ala Phe Ser Leu Arg His Thr Thr Glu Asn  
 420 425 430

Lys Pro His Ser Pro Lys Thr Pro Glu Pro Arg Arg Ser Pro Leu Gly  
 435 440 445

Gln Lys Arg Gly Met Leu Ser Ser Ser Thr Ser Gly Ala Ile Ser Asp  
 450 455 460

Lys Gly Val Leu Arg Pro Gln Lys Glu Ala Val Ser Ser Ser His Gly  
 465 470 475 480

Pro Ser Asp Pro Thr Asp Arg Ala Glu Val Glu Lys Asp Ser Gly His  
 485 490 495

Gly Ser Thr Ser Val Asp Ser Glu Gly Phe Ser Ile Pro Asp Thr Gly  
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Ser His Cys Ser Ser Glu Tyr Ala Ala Ser Ser Pro Gly Asp Arg Gly  
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Ser Gln Glu His Val Asp Ser Gln Glu Lys Ala Pro Glu Thr Asp Asp  
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Lys Arg Phe Lys Lys Glu Glu Ile Leu Ser Ser Ser Asp Ile Cys Gln  
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Lys Leu Val Asn Thr Gln Asp Met Ser Ala Ser Gln Val Asp Val Ala  
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Val Lys Ile Asn Lys Lys Val Val Pro Leu Asp Phe Ser Met Ser Ser  
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Gly Glu Gln Asn Tyr Arg Lys Phe Arg Ala Lys Ile Cys Pro Gly Glu  
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Asn Gln Ala Ala Glu Asp Glu Leu Arg Lys Glu Ile Ser Lys Thr Met  
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Phe Ala Glu Met Glu Ile Ile Gly Gln Phe Asn Leu Gly Phe Ile Ile  
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Thr Lys Leu Asn Glu Asp Ile Phe Ile Val Asp Gln His Ala Thr Asp  
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Glu Lys Tyr Asn Phe Glu Met Leu Gln Gln His Thr Val Leu Gln Gly  
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725 730 735

Ala Val Leu Ile Glu Asn Leu Glu Ile Phe Arg Lys Asn Gly Phe Asp  
740 745 750

Phe Val Ile Asp Glu Asn Ala Pro Val Thr Glu Arg Ala Lys Leu Ile  
755 760 765

Ser Leu Pro Thr Ser Lys Asn Trp Thr Phe Gly Pro Gln Asp Val Asp  
770 775 780

Glu Leu Ile Phe Met Leu Ser Asp Ser Pro Gly Val Met Cys Arg Pro  
785 790 795 800

Ser Arg Val Lys Gln Met Phe Ala Ser Arg Ala Cys Arg Lys Ser Val  
805 810 815

Met Ile Gly Thr Ala Leu Asn Thr Ser Glu Met Lys Lys Leu Ile Thr  
820 825 830

His Met Gly Glu Met Asp His Pro Trp Asn Cys Pro His Gly Arg Pro  
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<212> DNA

<213> Homo sapiens

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 35 40 45

Phe Asp Lys Ile Glu Val Arg Asp Asn Gly Glu Gly Ile Lys Ala Val  
 50 55 60

Asp Ala Pro Val Met Ala Met Lys Tyr Tyr Thr Ser Lys Ile Asn Ser  
 65 70 75 80

His Glu Asp Leu Glu Asn Leu Thr Thr Tyr Gly Phe Arg Gly Glu Ala  
 85 90 95

Leu Gly Ser Ile Cys Cys Ile Ala Glu Val Leu Ile Thr Thr Arg Thr  
 100 105 110

Ala Ala Asp Asn Phe Ser Thr Gln Tyr Val Leu Asp Gly Ser Gly His  
 115 120 125

Ile Leu Ser Gln Lys Pro Ser His Leu Gly Gln Gly Thr Thr Val Thr  
 130 135 140

Ala Leu Arg Leu Phe Lys Asn Leu Pro Val Arg Lys Gln Phe Tyr Ser  
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 195 200 205

Ala Leu Met Ser Val Leu Gly Thr Ala Val Met Asn Asn Met Glu Ser  
 210 215 220

Phe Gln Tyr His Ser Glu Glu Ser Gln Ile Tyr Leu Ser Gly Phe Leu  
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Pro Lys Cys Asp Ala Asp His Ser Phe Thr Ser Leu Ser Thr Pro Glu  
 245 250 255

Arg Ser Phe Ile Phe Ile Asn Ser Arg Pro Val His Gln Lys Asp Ile  
 260 265 270

Leu Lys Leu Ile Arg His His Tyr Asn Leu Lys Cys Leu Lys Glu Ser  
 275 280 285

Thr Arg Leu Tyr Pro Val Phe Phe Leu Lys Ile Asp Val Pro Thr Ala  
 290 295 300

Asp Val Asp Val Asn Leu Thr Pro Asp Lys Ser Gln Val Leu Leu Gln  
 305 310 315 320

Asn Lys Glu Ser Val Leu Ile Ala Leu Glu Asn Leu Met Thr Thr Cys  
 325 330 335

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Val Ser Ala Ala Asp Ile Val Leu Ser Lys Thr Ala Glu Thr Asp Val  
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Leu Phe Asn Lys Val Glu Ser Ser Gly Lys Asn Tyr Ser Asn Val Asp  
 370 375 380

Thr Ser Val Ile Pro Phe Gln Asn Asp Met His Asn Asp Glu Ser Gly  
 385 390 395 400

Lys Asn Thr Asp Asp Cys Leu Asn His Gln Ile Ser Ile Gly Asp Phe  
 405 410 415

Gly Tyr Gly His Cys Ser Ser Glu Ile Ser Asn Ile Asp Lys Asn Thr  
 420 425 430

Lys Asn Ala Phe Gln Asp Ile Ser Met Ser Asn Val Ser Trp Glu Asn  
 435 440 445

Ser Gln Thr Glu Tyr Ser Lys Thr Cys Phe Ile Ser Ser Val Lys His  
 450 455 460  
 Thr Gln Ser Glu Asn Gly Asn Lys Asp His Ile Asp Glu Ser Gly Glu  
 465 470 475 480  
 Asn Glu Glu Glu Ala Gly Leu Glu Asn Ser Ser Glu Ile Ser Ala Asp  
 485 490 495  
 Glu Trp Ser Arg Gly Asn Ile Leu Lys Asn Ser Val Gly Glu Asn Ile  
 500 505 510  
 Glu Pro Val Lys Ile Leu Val Pro Glu Lys Ser Leu Pro Cys Lys Val  
 515 520 525  
 Ser Asn Asn Asn Tyr Pro Ile Pro Glu Gln Met Asn Leu Asn Glu Asp  
 530 535 540  
 Ser Cys Asn Lys Lys Ser Asn Val Ile Asp Asn Lys Ser Gly Lys Val  
 545 550 555 560  
 Thr Ala Tyr Asp Leu Leu Ser Asn Arg Val Ile Lys Lys Pro Met Ser  
 565 570 575  
 Ala Ser Ala Leu Phe Val Gln Asp His Arg Pro Gln Phe Leu Ile Glu  
 580 585 590  
 Asn Pro Lys Thr Ser Leu Glu Asp Ala Thr Leu Gln Ile Glu Glu Leu  
 595 600 605  
 Trp Lys Thr Leu Ser Glu Glu Glu Lys Leu Lys Tyr Glu Glu Lys Ala  
 610 615 620  
 Thr Lys Asp Leu Glu Arg Tyr Asn Ser Gln Met Lys Arg Ala Ile Glu  
 625 630 635 640  
 Gln Glu Ser Gln Met Ser Leu Lys Asp Gly Arg Lys Lys Ile Lys Pro  
 645 650 655  
 Thr Ser Ala Trp Asn Leu Ala Gln Lys His Lys Leu Lys Thr Ser Leu  
 660 665 670  
 Ser Asn Gln Pro Lys Leu Asp Glu Leu Leu Gln Ser Gln Ile Glu Lys  
 675 680 685  
 Arg Arg Ser Gln Asn Ile Lys Met Val Gln Ile Pro Phe Ser Met Lys  
 690 695 700  
 Asn Leu Lys Ile Asn Phe Lys Lys Gln Asn Lys Val Asp Leu Glu Glu  
 705 710 715 720

## MOR0277.ST25.txt

Lys Asp Glu Pro Cys Leu Ile His Asn Leu Arg Phe Pro Asp Ala Trp  
725 730 735

Leu Met Thr Ser Lys Thr Glu Val Met Leu Leu Asn Pro Tyr Arg Val  
740 745 750

Glu Glu Ala Leu Leu Phe Lys Arg Leu Leu Glu Asn His Lys Leu Pro  
755 760 765

Ala Glu Pro Leu Glu Lys Pro Ile Met Leu Thr Glu Ser Leu Phe Asn  
770 775 780

Gly Ser His Tyr Leu Asp Val Leu Tyr Lys Met Thr Ala Asp Asp Gln  
785 790 795 800

Arg Tyr Ser Gly Ser Thr Tyr Leu Ser Asp Pro Arg Leu Thr Ala Asn  
805 810 815

Gly Phe Lys Ile Lys Leu Ile Pro Gly Val Ser Ile Thr Glu Asn Tyr  
820 825 830

Leu Glu Ile Glu Gly Met Ala Asn Cys Leu Pro Phe Tyr Gly Val Ala  
835 840 845

Asp Leu Lys Glu Ile Leu Asn Ala Ile Leu Asn Arg Asn Ala Lys Glu  
850 855 860

Val Tyr Glu Cys Arg Pro Arg Lys Val Ile Ser Tyr Leu Glu Gly Glu  
865 870 875 880

Ala Val Arg Leu Ser Arg Gln Leu Pro Met Tyr Leu Ser Lys Glu Asp  
885 890 895

Ile Gln Asp Ile Ile Tyr Arg Met Lys His Gln Phe Gly Asn Glu Ile  
900 905 910

Lys Glu Cys Val His Gly Arg Pro Phe Phe His His Leu Thr Tyr Leu  
915 920 925

Pro Glu Thr Thr  
930

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<211> 3063  
<212> DNA  
<213> Homo sapiens

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ctgctctgtt aaaagcgaaa atgaaacaat tgccctgcgc aacagttcga ctctttcaa 120  
gttctcagat catcacttcg tgggtcagtg ttgtaaaaga gcttattgaa aactccttgg 180  
atgctggtgc cacaagcgta gatgttaaac tggagaacta tggatttgat aaaattgagg 240

tgcgagataa cggggagggt atcaaggctg ttgatgcacc tgtaatggca atgaagtact	300
acacctcaaa aataaatagt catgaagatc ttgaaaattht gacaacttac ggthtttcgtg	360
gagaagcctt ggggtcaatt tgttgtatag ctgaggthttt aattacaaca agaacggctg	420
ctgataattht tagcacccag tatgtthttag atggcagtggt ccacatactt tctcagaaac	480
cttcacatct tgggtcaagggt acaactgtaa ctgctthtaag attattthtaag aatctacctg	540
taagaaagca gthtttactca actgcaaaaa aatgtaaaga tgaaataaaa aagatccaag	600
atctcctcat gagctthtgggt atcctthaaac ctgactthtaag gattgtcttht gtacataaca	660
aggcagttat ttggcagaaa agcagagtat cagatcacaa gatggctctc atgtcagttc	720
tggggactgc tgttatgaac aatatggaat cctthtcagta ccactctgaa gaatctcaga	780
thttatctcag tggattthctt ccaaagtgtg atgcagacca ctctthtact agtctthtcaa	840
caccagaaaag aagthttcatc thcataaaca gtcgaccagt acatcaaaaa gatathcttaa	900
agthtaatccg acatcattac aatctgaaat gcctaaagga atctactcgt ttgtatcctg	960
thttctthtct gaaaatcgat gthcttacag ctgatgttga tgtaaatthta acaccagata	1020
aaagccaagt attattacaa aataaggaat ctgtththtaat tgctcttgaa aatctgatga	1080
cgacttgtha tggaccatta cctagtacaa attctthtga aaataataaa acagatgttht	1140
ccgcagctga catcgthtctt agtaaaacag cagaaacaga tgtgctthttt aataaagtgg	1200
aatcatctgg aaagaattat tcaaathgttg atactthcagt cattccattc caaaatgata	1260
tgcataatga tgaatctgga aaaaacactg atgattgttht aaatcaccag ataagtattg	1320
gtgactthtgg thtatggatcat tgtagtagtg aaaththctaa cattgataaa aacactaaga	1380
atgcattthca ggacattthca atgagthaatg tatcatggga gaactctcag acggaatata	1440
gtaaaacttg thttataagt tccgttaagc acaccagtc agaaaatggc aataaagacc	1500
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ctgcagatga gtggagcagg ggaaatatac thaaaaatthc agtgggagag aatattgaaac	1620
ctgtgaaaat thtagtgctt gaaaaaagtht taccatgtaa agtaagthaat aataattatc	1680
caatccctga acaaatgaat ctthaatgaag attcatgtaa caaaaaatca aatgthaatg	1740
ataataaatc tggaaaagtht acagctthtga atthtactthag caatcgagtha atcaagaaac	1800
ccatgtcagc aagtgtctctt thtgtthcaag atcatcgthc tcagththtctc atagaaaatc	1860
ctaagactag thtagaggat gcaacactac aaattgaaga actgtggaag acattgagtg	1920
aagaggaaaa actgaaatat gaagagaagg ctactaaaga cttggaacga tacaatagtc	1980
aatgaagag agccattgaa caggagthcag aaatgtcact aaaagatggc agaaaaaaga	2040
taaaacccac cagcgcatgg aatthtggccc agaagcacaa gthtaaaaacc tcattatcta	2100
atcaacccaaa acttgatgaa thctthtctag cccaaattga aaaaagaagg agtcaaaata	2160
thaaaaatgg acagatcccc ththtctatga aaactthtaa aataaatthtt aagaaacaaa	2220
acaaagthtga cttagaagag aaggatgaac cttgctthgat ccacaatctc aggtthtctg	2280
atgcatggct aatgacatcc aaaacagagg thaatgtthatt aaatccatat agagtagaag	2340

## MOR0277.ST25.txt

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agccaattat gttaacagag agtcttttta atggatctca ttatttagac gttttatata 2460  
aatgacagc agatgaccaa agatacagt gatcaactta cctgtctgat cctcgtctta 2520  
cagcgaatgg tttcaagata aaattgatac caggagtttc aattactgaa aattacttgg 2580  
aatagaagg aatggcta atgtctcccat tctatggagt agcagattta aaagaaattc 2640  
ttaatgctat attaaacaga aatgcaaagg aagtttatga atgtagacct cgcaaagtga 2700  
taagttatit agagggagaa gcagtgcgtc tatccagaca attacccatg tacttatcaa 2760  
aagaggacat ccaagacatt atctacagaa tgaagcacca gtttggaat gaaattaaag 2820  
agtgtgttca tggctgcccc ttttttcatt atttaaccta tcttcagaa actacatgat 2880  
taaataatgt taagaagatt agttaccatt gaaattgggt ctgtcataaa acagcatgat 2940  
tctggtttta aattatcttt gtattatgtg tcacatgggt attttttaaa tgaggattca 3000  
ctgacttggt tttatattga aaaaagttcc acgtattgta gaaaacgtaa ataaactaat 3060  
aac 3063

<210> 11  
<211> 934  
<212> PRT  
<213> Homo sapiens

<400> 11

Met Ala Val Gln Pro Lys Glu Thr Leu Gln Leu Glu Ser Ala Ala Glu  
1 5 10 15

Val Gly Phe Val Arg Phe Phe Gln Gly Met Pro Glu Lys Pro Thr Thr  
20 25 30

Thr Val Arg Leu Phe Asp Arg Gly Asp Phe Tyr Thr Ala His Gly Glu  
35 40 45

Asp Ala Leu Leu Ala Ala Arg Glu Val Phe Lys Thr Gln Gly Val Ile  
50 55 60

Lys Tyr Met Gly Pro Ala Gly Ala Lys Asn Leu Gln Ser Val Val Leu  
65 70 75 80

Ser Lys Met Asn Phe Glu Ser Phe Val Lys Asp Leu Leu Leu Val Arg  
85 90 95

Gln Tyr Arg Val Glu Val Tyr Lys Asn Arg Ala Gly Asn Lys Ala Ser  
100 105 110

Lys Glu Asn Asp Trp Tyr Leu Ala Tyr Lys Ala Ser Pro Gly Asn Leu  
115 120 125

Ser Gln Phe Glu Asp Ile Leu Phe Gly Asn Asn Asp Met Ser Ala Ser  
130 135 140



## MOR0277.ST25.txt

Ile Gly Val Val Gly Val Lys Met Ser Ala Val Asp Gly Gln Arg Gln  
 145 150 155 160

Val Gly Val Gly Tyr Val Asp Ser Ile Gln Arg Lys Leu Gly Leu Cys  
 165 170 175

Glu Phe Pro Asp Asn Asp Gln Phe Ser Asn Leu Glu Ala Leu Leu Ile  
 180 185 190

Gln Ile Gly Pro Lys Glu Cys Val Leu Pro Gly Gly Glu Thr Ala Gly  
 195 200 205

Asp Met Gly Lys Leu Arg Gln Ile Ile Gln Arg Gly Gly Ile Leu Ile  
 210 215 220

Thr Glu Arg Lys Lys Ala Asp Phe Ser Thr Lys Asp Ile Tyr Gln Asp  
 225 230 235 240

Leu Asn Arg Leu Leu Lys Gly Lys Lys Gly Glu Gln Met Asn Ser Ala  
 245 250 255

Val Leu Pro Glu Met Glu Asn Gln Val Ala Val Ser Ser Leu Ser Ala  
 260 265 270

Val Ile Lys Phe Leu Glu Leu Leu Ser Asp Asp Ser Asn Phe Gly Gln  
 275 280 285

Phe Glu Leu Thr Thr Phe Asp Phe Ser Gln Tyr Met Lys Leu Asp Ile  
 290 295 300

Ala Ala Val Arg Ala Leu Asn Leu Phe Gln Gly Ser Val Glu Asp Thr  
 305 310 315 320

Thr Gly Ser Gln Ser Leu Ala Ala Leu Leu Asn Lys Cys Lys Thr Pro  
 325 330 335

Gln Gly Gln Arg Leu Val Asn Gln Trp Ile Lys Gln Pro Leu Met Asp  
 340 345 350

Lys Asn Arg Ile Glu Glu Arg Leu Asn Leu Val Glu Ala Phe Val Glu  
 355 360 365

Asp Ala Glu Leu Arg Gln Thr Leu Gln Glu Asp Leu Leu Arg Arg Phe  
 370 375 380

Pro Asp Leu Asn Arg Leu Ala Lys Lys Phe Gln Arg Gln Ala Ala Asn  
 385 390 395 400

Leu Gln Asp Cys Tyr Arg Leu Tyr Gln Gly Ile Asn Gln Leu Pro Asn  
 405 410 415

Val Ile Gln Ala Leu Glu Lys His Glu Gly Lys His Gln Lys Leu Leu  
 420 425 430

Leu Ala Val Phe Val Thr Pro Leu Thr Asp Leu Arg Ser Asp Phe Ser  
 435 440 445  
 Lys Phe Gln Glu Met Ile Glu Thr Thr Leu Asp Met Asp Gln Val Glu  
 450 455 460  
 Asn His Glu Phe Leu Val Lys Pro Ser Phe Asp Pro Asn Leu Ser Glu  
 465 470 475 480  
 Leu Arg Glu Ile Met Asn Asp Leu Glu Lys Lys Met Gln Ser Thr Leu  
 485 490 495  
 Ile Ser Ala Ala Arg Asp Leu Gly Leu Asp Pro Gly Lys Gln Ile Lys  
 500 505 510  
 Leu Asp Ser Ser Ala Gln Phe Gly Tyr Tyr Phe Arg Val Thr Cys Lys  
 515 520 525  
 Glu Glu Lys Val Leu Arg Asn Asn Lys Asn Phe Ser Thr Val Asp Ile  
 530 535 540  
 Gln Lys Asn Gly Val Lys Phe Thr Asn Ser Lys Leu Thr Ser Leu Asn  
 545 550 555 560  
 Glu Glu Tyr Thr Lys Asn Lys Thr Glu Tyr Glu Glu Ala Gln Asp Ala  
 565 570 575  
 Ile Val Lys Glu Ile Val Asn Ile Ser Ser Gly Tyr Val Glu Pro Met  
 580 585 590  
 Gln Thr Leu Asn Asp Val Leu Ala Gln Leu Asp Ala Val Val Ser Phe  
 595 600 605  
 Ala His Val Ser Asn Gly Ala Pro Val Pro Tyr Val Arg Pro Ala Ile  
 610 615 620  
 Leu Glu Lys Gly Gln Gly Arg Ile Ile Leu Lys Ala Ser Arg His Ala  
 625 630 635 640  
 Cys Val Glu Val Gln Asp Glu Ile Ala Phe Ile Pro Asn Asp Val Tyr  
 645 650 655  
 Phe Glu Lys Asp Lys Gln Met Phe His Ile Ile Thr Gly Pro Asn Met  
 660 665 670  
 Gly Gly Lys Ser Thr Tyr Ile Arg Gln Thr Gly Val Ile Val Leu Met  
 675 680 685  
 Ala Gln Ile Gly Cys Phe Val Pro Cys Glu Ser Ala Glu Val Ser Ile  
 690 695 700

## MOR0277.ST25.txt

Val Asp Cys Ile Leu Ala Arg Val Gly Ala Gly Asp Ser Gln Leu Lys  
705 710 715 720

Gly Val Ser Thr Phe Met Ala Glu Met Leu Glu Thr Ala Ser Ile Leu  
725 730 735

Arg Ser Ala Thr Lys Asp Ser Leu Ile Ile Ile Asp Glu Leu Gly Arg  
740 745 750

Gly Thr Ser Thr Tyr Asp Gly Phe Gly Leu Ala Trp Ala Ile Ser Glu  
755 760 765

Tyr Ile Ala Thr Lys Ile Gly Ala Phe Cys Met Phe Ala Thr His Phe  
770 775 780

His Glu Leu Thr Ala Leu Ala Asn Gln Ile Pro Thr Val Asn Asn Leu  
785 790 795 800

His Val Thr Ala Leu Thr Thr Glu Glu Thr Leu Thr Met Leu Tyr Gln  
805 810 815

Val Lys Lys Gly Val Cys Asp Gln Ser Phe Gly Ile His Val Ala Glu  
820 825 830

Leu Ala Asn Phe Pro Lys His Val Ile Glu Cys Ala Lys Gln Lys Ala  
835 840 845

Leu Glu Leu Glu Glu Phe Gln Tyr Ile Gly Glu Ser Gln Gly Tyr Asp  
850 855 860

Ile Met Glu Pro Ala Ala Lys Lys Cys Tyr Leu Glu Arg Glu Gln Gly  
865 870 875 880

Glu Lys Ile Ile Gln Glu Phe Leu Ser Lys Val Lys Gln Met Pro Phe  
885 890 895

Thr Glu Met Ser Glu Glu Asn Ile Thr Ile Lys Leu Lys Gln Leu Lys  
900 905 910

Ala Glu Val Ile Ala Lys Asn Asn Ser Phe Val Asn Glu Ile Ile Ser  
915 920 925

Arg Ile Lys Val Thr Thr  
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<211> 3145

<212> DNA

<213> Homo sapiens

<400> 12

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gtttcgacat ggcggtgcag ccgaaggaga cgctgcagtt ggagagcgcg gccgaggtcg 120

gcttcgtgcg cttctttcag ggcattgccg agaagccgac caccacagtg cgccttttcg	180
accggggcga cttctatacg gcgcacggcg aggacgcgct gctggccgcc cgggaggtgt	240
tcaagacca gggggtgatc aagtacatgg ggccggcagg agcaaagaat ctgcagagtg	300
ttgtgcttag taaaatgaat tttgaatctt ttgtaaaaga tcttcttctg gttcgtcagt	360
atagagttga agtttataag aatagagctg gaaataaggc atccaaggag aatgatttgt	420
atttggcata taaggcttct cctggcaatc tctctcagtt tgaagacatt ctctttggta	480
acaatgatat gtcagcttcc attggtgttg tgggtgttaa aatgtccgca gttgatggcc	540
agagacaggt tggagttggg tatgtggatt ccatacagag gaaactagga ctgtgtgaat	600
tccctgataa tgatcagttc tccaatcttg aggctctcct catccagatt ggaccaaagg	660
aatgtgtttt acccgaggga gagactgctg gagacatggg gaaactgaga cagataattc	720
aaagaggagg aattctgatc acagaaagaa aaaaagctga cttttccaca aaagacattt	780
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aaaaagataa acagatgttc cacatcatta ctggcccaa tatgggaggt aaatcaacat	2100
atattcgaca aactggggtg atagtactca tggcccaa atgggtgttt gtgcatgtg	2160
agtcagcaga agtgtccatt gtggactgca tcttagcccg agtaggggct ggtgacagtc	2220

## MOR0277.ST25.txt

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atatttagta atattttact ttgaggacat tttcaaagat ttttattttg aaaaatgaga 3060
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<210> 13
<211> 756
<212> PRT
<213> Homo sapiens

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<400> 13

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Met Ser Phe Val Ala Gly Val Ile Arg Arg Leu Asp Glu Thr Val Val
1          5          10          15

```

```

Asn Arg Ile Ala Ala Gly Glu Val Ile Gln Arg Pro Ala Asn Ala Ile
          20          25          30

```

```

Lys Glu Met Ile Glu Asn Cys Leu Asp Ala Lys Ser Thr Ser Ile Gln
          35          40          45

```

```

Val Ile Val Lys Glu Gly Gly Leu Lys Leu Ile Gln Ile Gln Asp Asn
          50          55          60

```

```

Gly Thr Gly Ile Arg Lys Glu Asp Leu Asp Ile Val Cys Glu Arg Phe
65          70          75          80

```

```

Thr Thr Ser Lys Leu Gln Ser Phe Glu Asp Leu Ala Ser Ile Ser Thr
          85          90          95

```

```

Tyr Gly Phe Arg Gly Glu Ala Leu Ala Ser Ile Ser His Val Ala His
          100          105          110

```

```

Val Thr Ile Thr Thr Lys Thr Ala Asp Gly Lys Cys Ala Tyr Arg Ala
          115          120          125

```

Ser Tyr Ser Asp Gly Lys Leu Lys Ala Pro Pro Lys Pro Cys Ala Gly  
 130 135 140

Asn Gln Gly Thr Gln Ile Thr Val Glu Asp Leu Phe Tyr Asn Ile Ala  
 145 150 155 160

Thr Arg Arg Lys Ala Leu Lys Asn Pro Ser Glu Glu Tyr Gly Lys Ile  
 165 170 175

Leu Glu Val Val Gly Arg Tyr Ser Val His Asn Ala Gly Ile Ser Phe  
 180 185 190

Ser Val Lys Lys Gln Gly Glu Thr Val Ala Asp Val Arg Thr Leu Pro  
 195 200 205

Asn Ala Ser Thr Val Asp Asn Ile Arg Ser Ile Phe Gly Asn Ala Val  
 210 215 220

Ser Arg Glu Leu Ile Glu Ile Gly Cys Glu Asp Lys Thr Leu Ala Phe  
 225 230 235 240

Lys Met Asn Gly Tyr Ile Ser Asn Ala Asn Tyr Ser Val Lys Lys Cys  
 245 250 255

Ile Phe Leu Leu Phe Ile Asn His Arg Leu Val Glu Ser Thr Ser Leu  
 260 265 270

Arg Lys Ala Ile Glu Thr Val Tyr Ala Ala Tyr Leu Pro Lys Asn Thr  
 275 280 285

His Pro Phe Leu Tyr Leu Ser Leu Glu Ile Ser Pro Gln Asn Val Asp  
 290 295 300

Val Asn Val His Pro Thr Lys His Glu Val His Phe Leu His Glu Glu  
 305 310 315 320

Ser Ile Leu Glu Arg Val Gln Gln His Ile Glu Ser Lys Leu Leu Gly  
 325 330 335

Ser Asn Ser Ser Arg Met Tyr Phe Thr Gln Thr Leu Leu Pro Gly Leu  
 340 345 350

Ala Gly Pro Ser Gly Glu Met Val Lys Ser Thr Thr Ser Leu Thr Ser  
 355 360 365

Ser Ser Thr Ser Gly Ser Ser Asp Lys Val Tyr Ala His Gln Met Val  
 370 375 380

Arg Thr Asp Ser Arg Glu Gln Lys Leu Asp Ala Phe Leu Gln Pro Leu  
 385 390 395 400

## MOR0277.ST25.txt

Ser Lys Pro Leu Ser Ser Gln Pro Gln Ala Ile Val Thr Glu Asp Lys  
 405 410 415  
 Thr Asp Ile Ser Ser Gly Arg Ala Arg Gln Gln Asp Glu Glu Met Leu  
 420 425 430  
 Glu Leu Pro Ala Pro Ala Glu Val Ala Ala Lys Asn Gln Ser Leu Glu  
 435 440 445  
 Gly Asp Thr Thr Lys Gly Thr Ser Glu Met Ser Glu Lys Arg Gly Pro  
 450 455 460  
 Thr Ser Ser Asn Pro Arg Lys Arg His Arg Glu Asp Ser Asp Val Glu  
 465 470 475 480  
 Met Val Glu Asp Asp Ser Arg Lys Glu Met Thr Ala Ala Cys Thr Pro  
 485 490 495  
 Arg Arg Arg Ile Ile Asn Leu Thr Ser Val Leu Ser Leu Gln Glu Glu  
 500 505 510  
 Ile Asn Glu Gln Gly His Glu Val Leu Arg Glu Met Leu His Asn His  
 515 520 525  
 Ser Phe Val Gly Cys Val Asn Pro Gln Trp Ala Leu Ala Gln His Gln  
 530 535 540  
 Thr Lys Leu Tyr Leu Leu Asn Thr Thr Lys Leu Ser Glu Glu Leu Phe  
 545 550 555 560  
 Tyr Gln Ile Leu Ile Tyr Asp Phe Ala Asn Phe Gly Val Leu Arg Leu  
 565 570 575  
 Ser Glu Pro Ala Pro Leu Phe Asp Leu Ala Met Leu Ala Leu Asp Ser  
 580 585 590  
 Pro Glu Ser Gly Trp Thr Glu Glu Asp Gly Pro Lys Glu Gly Leu Ala  
 595 600 605  
 Glu Tyr Ile Val Glu Phe Leu Lys Lys Lys Ala Glu Met Leu Ala Asp  
 610 615 620  
 Tyr Phe Ser Leu Glu Ile Asp Glu Glu Gly Asn Leu Ile Gly Leu Pro  
 625 630 635 640  
 Leu Leu Ile Asp Asn Tyr Val Pro Pro Leu Glu Gly Leu Pro Ile Phe  
 645 650 655  
 Ile Leu Arg Leu Ala Thr Glu Val Asn Trp Asp Glu Glu Lys Glu Cys  
 660 665 670  
 Phe Glu Ser Leu Ser Lys Glu Cys Ala Met Phe Tyr Ser Ile Arg Lys  
 675 680 685

Gln Tyr Ile Ser Glu Glu Ser Thr Leu Ser Gly Gln Gln Ser Glu Val  
690 695 700

Pro Gly Ser Ile Pro Asn Ser Trp Lys Trp Thr Val Glu His Ile Val  
705 710 715 720

Tyr Lys Ala Leu Arg Ser His Ile Leu Pro Pro Lys His Phe Thr Glu  
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Ala Gly Ala Thr Asn Ile Asp Leu Lys Leu Lys Asp Tyr Gly Val Asp  
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Leu Ile Glu Val Ser Asp Asn Gly Cys Gly Val Glu Glu Glu Asn Phe  
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Glu Gly Leu Thr Leu Lys His His Thr Ser Lys Ile Gln Glu Phe Ala  
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